

## Oral Presentations

## Workshop 8. Microbial communities: Relationships and disease

S17

**WS8.5** **Airway bacterial community structure and correlation during health and disease**

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**Objectives:** Ecological relationships between bacteria in communities may contribute to disease progression. Our aim was to compare bacterial community structures in CF airways and the upper airways of healthy volunteers as a surrogate for a healthy lung microbiome.

**Methods:** CF sputum samples (analysed by pyrosequencing) were compared with samples from 9 sites in the upper airways (Human Microbiome Project; sub- and supragingival-plaque, saliva, buccal mucosa, hard palate, keratinised gingiva, tongue dorsum, tonsils and throat). Normalised data for each cohort was analysed for occupancy and relative abundance of different taxa. Significance of bacterial co-occurrence was determined using Spearman's Ranked Correlation Coefficient with a cut-off of  $>0.5$  ( $p < 0.001$ ).

**Results:** Preliminary analysis demonstrates a "core" community with members of the genera *Streptococcus*, *Actinomyces*, *Fusobacterium*, *Gemella*, *Granulicatella*, *Neisseria*, *Prevotella*, *Rothia* and *Veillonella* the most frequently detected and abundant taxa, irrespective of host state. There was an increased prevalence of *Pseudomonas* and *Burkholderia* species in CF airways. Furthermore, a significant co-occurrence was detected between a number of the "core" taxa, which formed sub-networks within the overall community structure.

**Conclusion:** A "core" microbial community is distributed throughout the airways. Due to a lack of resolution in short-read sequence data, it is difficult to assess if a shift within the "core" taxa at the species level contributes to disease progression. Further detailed analysis of inter- and intra community architecture is on-going to confirm these findings.

**WS8.6** **Interaction of microorganisms modulating the cystic fibrosis clinical severity**

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**Objectives:** To evaluate the interaction of *P. aeruginosa* mucoid (PAM) and non-mucoid (PANM), *Staphylococcus aureus* (SA), *Burkholderia cepacia* (BC), *Achromobacter xylosoxidans* (AX), and *CFTR* mutation as modulators of Cystic Fibrosis (CF).

**Methods:** 180 patients were included. Bacterial identification was performed by specialists. Clinical variables: sex, race, scores [Shwachman-Kulczycki (SK), Kanga and Bhalla (BS)], BMI, patient age, diagnosis age, onset of symptoms lung, SaO<sub>2</sub>, spirometry (FVC, FEV<sub>1</sub>, FEV<sub>1</sub>/FVC, FEF<sub>25-75</sub>%), comorbidities (osteoporosis and diabetes mellitus). Statistical analysis: MDR2.0 and MDRPT0.4.7. Numerical data: classified by the median. Categorical data: presence or absence (comorbidities). BS was associated with the interaction of PAM, PANM, SA and *CFTR* ( $p = 0-0.0001$ ), and SK with PAM, PANM, AX, BC and *CFTR* ( $p = 0.05-0.051$ ). FVC was associated with PAM and AX ( $p = 0.034$ ), the FEV<sub>1</sub>/FVC and FEF<sub>25-75</sub>% with PAM and PANM ( $p = 0.004-0.005$ ,  $p = 0.003-0.004$ , respectively) and FEV<sub>1</sub> with PANM, PAM and BC ( $p = 0.001-0.002$ ). Time of diagnosis was associated with PAM, PANM, AX, SA, BC and *CFTR* ( $p = 0-0.0001$ ), while the patient age with PANM and *CFTR* ( $p = 0.038-0.039$ ), and the first clinical manifestation with BC and *CFTR* ( $p = 0-0.001$ ). The influence of multiple factors associated with the CF severity is importance for understanding the pathophysiology of diseases with complex phenotypic expression. In CF, one of the factors associated with the severity is the presence of bacteria in the lung, but little is known about the joint action of different microorganisms in the clinical severity, and the interaction between them is not reported.

**Conclusion:** Bacterial interaction was associated with CF severity.